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514 AGAGAGCCCTGCCACAGAGGAGGATCTAGAGAGGCACTTCGGCTATAGTGGCTTTCG 5314
458 ----- CTTGCTGGCTCCACAGGTTCAAACTTCCAGCAGCTTTTACACTGTGAGG 513
5313 CGAACTCTGCTGGCTCCACTACTT- TAACTTCCAGTGGCTTTTGTACACTGTGAGG 5255
514 GTAAGACCATCTACTCAAGCTCAGCTCAGCTGAGCGGATGCCCTCTCCACCAAGCTCGAG 573
5254 GGAAGACTGCTTACTTCAAGCTCAGCTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 5195
574 TGTCCTGCTCAACTCAGA-TGCTGTGATAGCAGTGAAGATTTCAGTGGATCTT 632
5194 CATTCCAGGTGACTTCAGACTGCTGCACTGGCAGTGAGAAATTCAGCCAGTGGATCT 5135
633 AGCTTGTGCTGGCTCGTGGGGTGGGACCGCTGAACCCAGAC 674
5134 AGCTTACTGGCTCCATGGGAGTGGGATCCACCGAGCTAGAC 5093

RESULT 4
US-08-592-126-114
Sequence 114, Application US/08592126
Patent No. 5821091
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 413 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: H505.seq
US-08-592-126-114

Query Match 7.8%; Score 135.4; DB 1; Length 413;
Best Local Similarity 82.0%; Pred. No. 7.9e-32;
Matches 168; Conservative 0; Mismatches 36; Indels 1; Gaps 1;
450 TCGGGAGCTGTGGTGGGCTCCACCCAGTTCACAACTCCACGAGCTTTGTTTACACTGT 509
209 TTGCTGAGCTGGGTGAGCTTCGCCAGTTCACAGTTCCTCTGTCGATGATATACACTGT 268

QY 510 GAGGTAACCACTACTCAAGCTTCAGCAATGGGGATGCACCTCTCCACCAAGCT 569
Db 269 GAGGGTAACCACTACTCAAGCTTCAGCAATGGGGATGCACCTCTCCACCAAGCT 328
QY 570 CGAGTGTCCAGCTCAACCTCAGA-TGCTGTGATAGCAGTGAAGATTTCACCCAGTGA 628
Db 329 TGAGTGGCCAGCTCTACTTCAGACTGTGCTGTCGACAGAAATTCACCAAGTGA 388
QY 629 TCTAGCTTGTGGCTCCGCTGGG 653
Db 389 TCTAGCTTGTGGCTTCTTGGG 413

RESULT 5
US-09-168-595-114
Sequence 114, Application US/09168595
Patent No. 655666
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/168,595
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 38/592,126
APPLICATION NUMBER: 38/592,126
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 413 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: H505.seq
US-09-168-595-114

Query Match 7.8%; Score 135.4; DB 4; Length 413;
Best Local Similarity 82.0%; Pred. No. 7.9e-32;
Matches 168; Conservative 0; Mismatches 36; Indels 1; Gaps 1;
450 TCGGGAGCTGTGGTGGGCTCCACCCAGTTCACAACTCCACGAGCTTTGTTTACACTGT 509
209 TTGCTGAGCTGGGTGAGCTTCGCCAGTTCACAGTTCCTCTGTCGATGATATACACTGT 268
QY 510 GAGGTAACCACTACTCAAGCTTCAGCAATGGGGATGCACCTCTCCACCAAGCT 569
Db 269 GAGGGTAACCACTACTCAAGCTTCAGCAATGGGGATGCACCTCTCCACCAAGCT 328

/tissue_type="Purified pancreatic islet"
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/clone_lib="HR85 islet"
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NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size selected on agarose gel. Average insert size ~4kb. 5'
XhoI site was destroyed after directional cloning
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
147 a 175 c 175 g 125 t

Query Match 13.2%; Score 229.8; DB 13; Length 622;
Best Local Similarity 84.9%; Pred. No. 2.6e-37;
Matches 269; Conservative 0; Mismatches 47; Indels 1; Gaps 1;
QY 146 GGAGGCTCGGACAAACAAAGATTGCTGCTGCTTCTACTATGGAGCTTGTGCCAGA 205
DB 620 GGAGGCTCGAGACACCAAGATTGCTGCTGCTTCTTCTGCTGAGGCTTGTGCCAGA 561
QY 206 AGGACACCCGACAGATGCCGGGACAGAGCTCTCTGTATGTGTGTCTGTAGGCCCTACT 265
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QY 266 GTGAGGTGCTCAGTCTGCTACACGGGGGTGAGGACCCACTTGTAGGAGGAGTCT 325
DB 500 GGGAGGTGCTCC-CAGTCAGAGGATGAGGTGAGGAAACCCACTTGTAGGAGGAGTCT 442
QY 326 GTCTCTATCAGAGCTCGAATGCTGTGGGAGAAATGCTGCTCTCTTTAGAGCTGTCA 385
DB 441 GTCCCTTAGCAGAGCTCAATGTTGCTGGAGATCTGCTCTCTTTCAGAGCTGSCA 382
QY 386 GGCAGGAGGTTTAACTGCTGAGAGCTGTGCTGCTGAGCGGCCCTTCCCGACGTGTC 445
DB 381 GGCAGGAGGTTTAACTGCTGAGAGCTGTGCTGCTGAGCTGTGCCACAGCGGCCCTTCCCGAGTGTCT 322
QY 446 TGTCTCGGGAGCTGTG 462
DB 321 TGTCCAGGAGATGGG 305

RESULT 13
CD516587
LOCUS
DEFINITION AGENCOURT 143658752 NIH MGC 181 Homo sapiens cDNA clone
IMAGE:30408298.5', mRNA sequence.
CD516587 790 bp mRNA linear EST 06-JUN-2003
CD516587.1 GI:31448305
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 790)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM491 row: a column: 11

High quality sequence stop: 702.
Location/Qualifiers
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/clone="IMAGE:30408298"
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/dev_stage="Unknown"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH MGC 181"
/notes="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
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insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH MGC Library."
BASE COUNT 160 a 216 c 221 g 193 t
ORIGIN
Query Match 13.2%; Score 229.2; DB 14; Length 790;
Best Local Similarity 67.2%; Pred. No. 3.5e-37;
Matches 430; Conservative 0; Mismatches 98; Indels 112; Gaps 3;
QY 145 CGGAGGCTGAGGAAACAAAGATTGCTGCTGCTTCTTCTACTCTGTGGAGCTTGTGCCAG 204
DB 76 CAGAGGCTGCAGAACACAGAAAGATTGCTGCTGCTTCTTCTCTCTGAAAGCTTGTGCCAG 135
QY 205 AAGGACACCCGACAGATGCCGGGACAGAGCTCTCTGTATGTGTGTCTGTAGGCCCTTAC 264
DB 136 AGGGGCACTCACCAGATGCCAGATGCCAGCTGCTGCTGTATGTATGTCTGTACGCCCTAC 195
QY 265 TGTGAGTGTCTCCAGTCTAGGTACACGGGGGTGAGGACCCACTTGTAGGAGGAGTCT 324
DB 196 TGGAGGTGTCTCC-CATTCAGAGACATGGGGGTGAGAGACCCACTTGTAGGAGGAGTCT 254
QY 325 TGTCTGTATCAGATCTCGAATGCTGTGTGGAGAAATGCTGTCTCTTTAGAGTGTCT 384
DB 255 TGACCTCTTAGCAGAGCTCGAACTCTGTGTGGAGATCTGCTGCTCTTTCAGAGCCCTC 314
QY 385 AGCGAGGAGCTTTAAAGTCTGCTGAAGTGTGCTGCTGACGCGGCCCTTCCCGACGTGCT 444
DB 315 AGCGAGGAGCTTTAAAGTCTGCTGAAGTGTGCTGACGCGGCCCTTCCCGACGTGCT 374
QY 445 CTGCTGAGGAGCTGTGTGGGCTCCA----- 472
DB 375 CTGTCAGGAGATGGGGTTCATCATAAGCCCTGATTTGGGGCTGCTGCTTTT 434
QY 473 ----- 472
DB 435 CAGAGATGCCCTGCCAGAGAGAGAAATCTAGAGAGGTAGTGTGCCACAGTGTCTTG 494
QY 475 -----CCAGTTCAAACCTTCCAGACAGCTTGTCTTACACTGTGAGGG 514
DB 495 CTGAGTGTGGGTGTGCTCCACCTGTCAAACCTTCCGCTGCTTGTCTTACCTTTCAGGG 554
QY 515 TAAACCATCTACTCAAGCTCAGCAATGCGGATGCACTCTCTCCACAGATGCTGAGT 574
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DB 675 GCTTGTGGGCTGTGGGGGTGGGACACACTGAGCCAGA 714

RESULT 14
AQ016709/c
LOCUS
DEFINITION AQ016709 536 bp DNA linear GSS Ag-JUN-1998
CIT-HSP-2301123.TR CIT-HSP Homo sapiens genomic clone 2301123,
genomic survey sequence.

ACCESSION A0016709
VERSION A0016709.1 GI:3195445
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 536)
ADAMS,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Sub,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished
COMMENT Other GSSs: CIT-HSP-2301I23.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: madams@igr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="2301I23"
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HindIII"
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ORIGIN

Query Match 13.0%; Score 226; DB 28; Length 536;
Best Local Similarity 84.0%; Pred. No. 1.6e-36;
Matches 267; Conservative 0; Mismatches 50; Indels 1; Gaps 1;
QY 145 CGAGGCTCGGAGACAAACAAAGATTCCTGCTTCCTACCTCGGAGCTTTGCCAG 204
DB 519 CAGAGGCTCGAGACAGCAAAAGATTGCTGCTATTCCTTCCTCGAAGCTTCATCCAA 460
QY 205 AAGGACCCCGCCAGATCGCGGAGAGCTCTCTGATGCTGCTGCTAGGCCCTTAC 264
DB 459 AGGGGACCCACAGATCGACACAGAGCTCTCTGATGAGTGTCTGTGACCCCTGC 400
QY 265 TGTGAGGTCTCTCCAGTCTGGGTACACGGGGGGGTGAGGAGCCCACTTCAGGAGGAGTC 324
DB 399 TGAAGGTATCTCC-CAGTCAGGAGGAGCATGGGTGTGAGGAGCCCACTTCAGGAGGAGTC 341
QY 325 TGTCTGTATCAGAGCTGAAATGCTGTGTGGAGAAATGCTGCTCTTTAGAGCTGTC 384
DB 340 TGTCTCTTAAACAGAGCTTGAGTGTGTGATGGGAGATCTGCTCTCTTCAGAGCTGTC 281
QY 385 AGGCAGGAGCTTTAAGTCTGCTGAAGCTGTGCTGAGCGGCCCTTCCCGCCAGCTGCT 444
DB 280 AGGCAGGAGCTTTAAGTCTGCTGAAGCTGTGCTGAGCGGCCCTTCCCGCCAGCTGCT 221
QY 445 CTCTCTCGGGGAGCTGTG 462
DB 220 CTGTCCAGGAGATGGG 203

RESULT 15
BX476445/c
LOCUS BX476445 420 bp mRNA linear EST 12-JUN-2003

DEFINITION DKFZp686D12186 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686D12186 5', mRNA sequence.
ACCESSION BX476445
VERSION BX476445.1 GI:31673701
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 420)
Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
AUTHORS EST (Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
TITLE Unpublished
JOURNAL
COMMENT Contact: Koehler K
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-
Heine-University, Duesseldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No sl sequence available.
This clone (DKFZp686D12186) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
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CDNA-collection"
BASE COUNT 100 a 121 c 124 g 75 t
ORIGIN

Query Match 12.7%; Score 220.6; DB 13; Length 420;
Best Local Similarity 82.8%; Pred. No. 2.2e-35;
Matches 264; Conservative 0; Mismatches 54; Indels 1; Gaps 1;
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DB 346 CAGAGGCTCGAGACAGCAAAAGATTCCTGCTTCCTTCCTCGAAGCTTTGCCAG 287
QY 205 AAGGACCCCGCCAGATCGCGGAGAGCTCTCTGATGCTGCTGAGGCCCTTAC 264
DB 286 AGGGGACCCACAGATTCGCCAGCCAGAGCTCTCTGATGAGTGTCTGTGCGGCCCTAT 227
QY 265 TGTGAGGTCTCTCCAGTCTGGGTACACGGGGGGGTGAGGAGCCCACTTCAGGAGGAGTC 324
DB 226 TGAAGGTGTCTCC-CAGTCAGGATACCTGGGTGTGAGGAGCCCACTTCAGGAGGAGTC 168
QY 325 TGTCTGTATCAGAGCTGAAATGCTGTGCTGGGAGAAATTCCTGCTCTTTAGAGCTGTC 384
DB 167 TGTCTCTTATCGAGCTTGAACATGCTGTGTGAGATCCACTCTCTCTTCAGTGTGCTCC 108
QY 385 AGGCAGGAGCTTTAAGTCTGCTGAAGCTGTGCTGAGCGGCCCTTCCCGCCAGCTGCT 444
DB 107 AGGCAGGAGCTTTAAGTCTGCTGAAGCTGTGCTGAGCGGCCCTTCCCGCCAGCTGCT 48
QY 445 CTGTCTCGGGGAGCTGTG 463
DB 47 CTGTCCAGGAGATGGG 29

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